



Explanation of functions

- 1 Chooses the device name of the DAQ or Sim mode
- 2 Enables to GUI to automatically detect the device. Automatically goes to Sim mode if device unavailable
- 3 Displays the value of the tested impedance
- 4 Specifies the sample rate (100kHz default)
- 5 Chooses the pulse type: Bipolar mode outputs a positive then negative pulse, monopolar outputs one pulse, either positive or negative (chosen from drop-down list)
- 6 Pulse amplitude: outputs the value displayed in volts, then gets sent to the stimulator. We recommend choosing 1mA/V setting on the stimulator to match the desired stimulating amplitude in mA
- 7 Specifies the number of pulses in the train pulse
- 8 Pulse width in μ s. If bipolar pulse is chosen in 5, the total duration of the pulse is doubled (for example 100 μ s positive and 100 μ s negative in the example shown in the screenshot)
- 9 Specifies the time between pulses
- 10 Waiting time before sending the pulse train
- 11 Knob specifying the amplitude of the voltage outputted to the stimulator, similar to 6

- 12 Minimum voltage sent to stimulator in recruitment curve
- 13 Maximum voltage sent to stimulator in recruitment curve
- 14 Step size for recruitment curve
- 15 Time between pulses in recruitment curve in seconds
- 16 Outputs 3 consecutive pulses of the sample amplitude for each amplitude in the recruitment curve
- 17 Introductory filename
- 18 Treatment state: Pre, Active or Post.
- 19 Autosaves the data after collection
- 20 Saves data in a struct array to minimize the file size
- 21 Notes for the user
- 22 Shows the directory of the loaded file
- 23 M/H cutoff in ms for M and H peak detections
- 24 Trial number, increases automatically
- 25 Directory of saved file
- 26 Plot showing the first pulse of the pulse train
- 27 Plot showing the entire pulse train
- 28 Plot showing the entire pulse train and record